

Fig. 1

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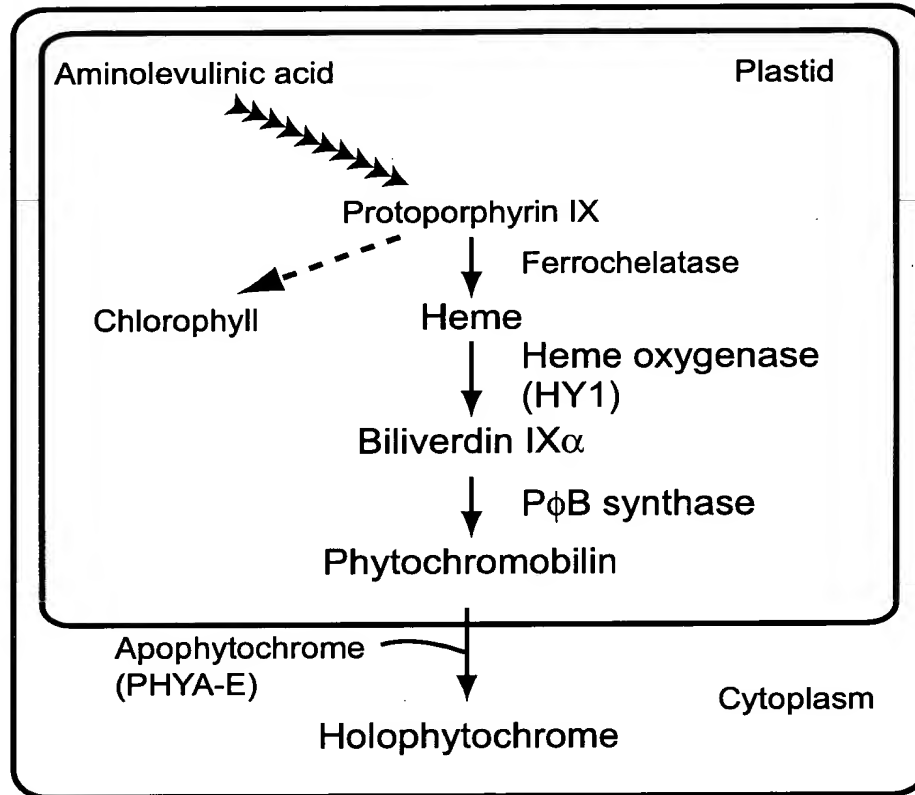
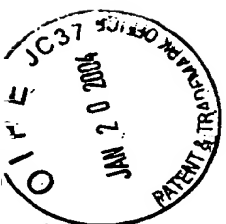


Fig. 2



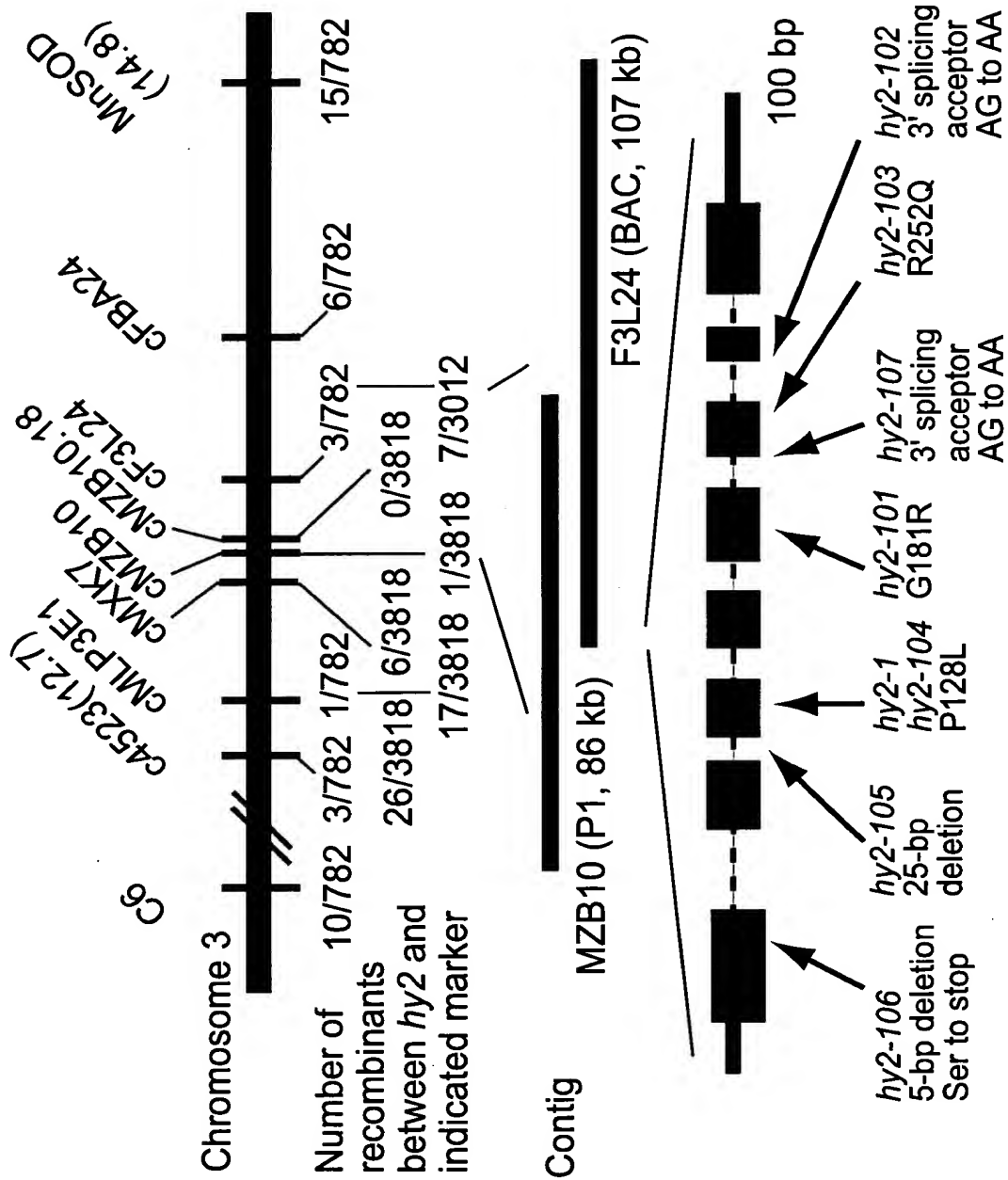
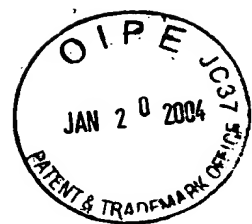


Fig. 3A



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gaattccccacgtcaacgtgactgtgcattccacgtggcggatgtggccctatagttgg 60
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aactgtgaaattttatctcttttatagataaAGAATCTTGCTTTTTCAGTTTTCAGTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTTGGTTTCAGTTTGTGAGTCT 240
TGTGTGAATGGCTTTATCAATGGAGTTTGGGTTTTCATTTGGGTCATGCTTCAAGGCACC 300
H A L S M E F G F S I G S C F K A P
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTCACGTTGAGAAGGAG 360
N P P V L I S A S P N K I N P T L R R R
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGCTATATAAGGAATTCGCAGAGTCTGC 420
hy2-106 *****
K K R F L L R V S A V S Y K E F A E S A
TTTAGAAGAAACCAGGAAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgcaat 480
L E E T R K R I V L E P S H L Q
taccatttctgttagttagtggaggatttatattctcattgtttcttgcgtgtgaattttg 540
ggttaattgatttgagttgtcattaggaaccaacaataactttactgttatagactgc 600
ttatataagtaaaagttcagattttgtttttctaatcacgaactgtttcagGAAAAGTA 660
E K Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCAAAATGCTTGTCTTTAAATCTTC 720
S S M T G L D G K T E L Q M L A F K S S
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K I R L L R S M A I E N E T M Q
gcagtacaaactgattgttttagtccatttcttactttcaattgattgattgtttgta 840
hy2-105 *****
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hy2-1, hy2-106 T
V F D F A G F M E P E Y D T P I F
TCTGTGCTAACTTTTTCACATCTACCAACGTTAACATAGTTGTATTgttaagtatatctt 960
C A N F F T S T N V N I V V L
agttatgctggagttatcaggctctgtattgtccaaactgatgttcaatattttactgtat 1020
gttctctcttagGGACCTTAATCCTTTGCATCAGTTGACTGACCAGCGGATTACCAAGA 1080
D L N P L H Q L T D Q T D Y Q D
CAAGTATTATAACAAGATAATGTCCATATATCACAAATATGCTGAGgtgaccacaagaat 1140
K Y Y N K I M S I Y H K Y A E
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hy2-101 A
T F P W G G K L T G E S I K F F
TCGCCTTTGGTGATGTGGACTAGGTTTTCGTCTAGCAAAGAAAAACATAAGGCTTTGTTT 1320
S P L V M W T R F S S S K E K E K A L F
TCTGCGTTTCTAGAGTACTATCAGgtatatactcagcgcccaaaagctaagggttttattg 1380
S A F L E Y Y Q
gaaactttgactgagaatctatcatcttcttctacagGCATGGCTTGAGATGACAATCC 1440
hy2-107 a
A W L E M T I Q
AAGTGAGGGAGGAGATGGAACCATCTCATGTGAGAGCCAATGTGAAGCACAACACAAGT 1500
V R E E M E P S H V R A N C E A Q E K Y
ACCTGACATGGCGAGCACAAAAGgtgatttcatttctttgtgtaatttgcaggttttga 1560
hy2-103 A
L T W R A Q K
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hy2-102 a
D P G
CATGGTCTTCTTAAAGATTAGTAGGTGAAGCAAAGGCAAAGgtatataaagatttgcac 1680
H G L L K R L V G E A K A K
cattagtgccccattattaattagcttgtgaagatgttgaaaatgatttgaacaaaatc 1740

Fig. 3B

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1.35 kb

Col
hy2-105
hy2-103
hy2-104
hy2-101
Ler
hy2-1
hy2-106
Ws
hy3-107

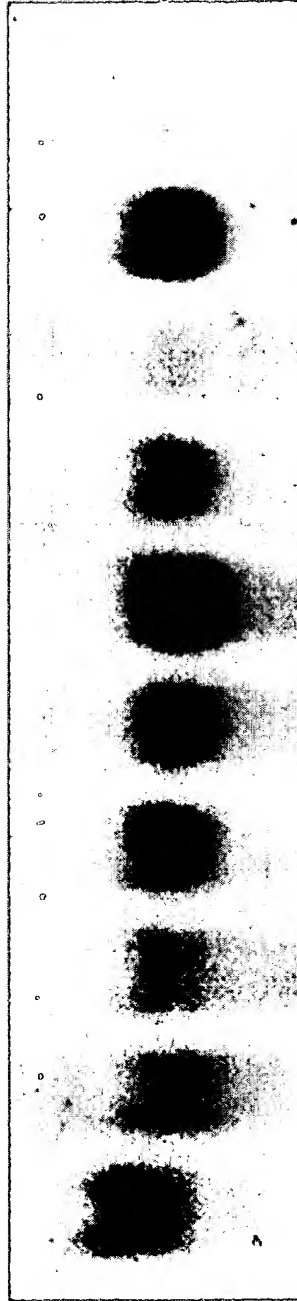


Fig. 4A

rRNA

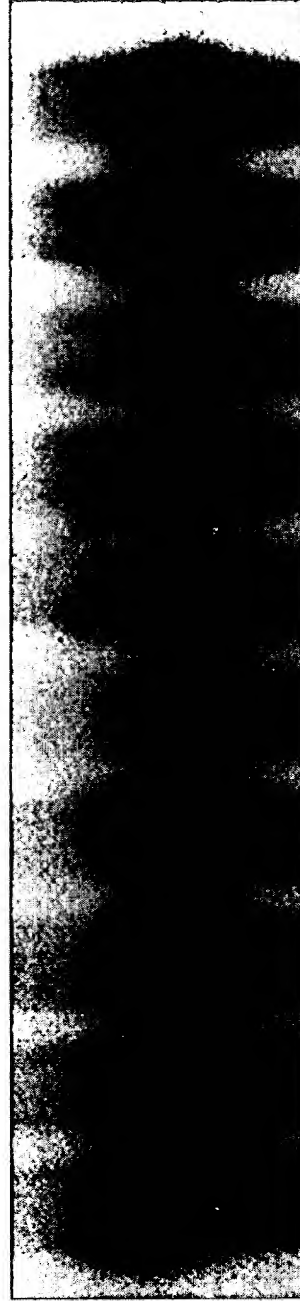


Fig. 4B

HY2 ARATH : MALSMEFGFSIGSCFKAPNPVLIASPNKINFTLRRRKKRRFLRVSASVKEFAESALETTRKRIVLEFSSHQEKYSSTMTGLDGK- : 80
YCP2_SYNPY : -----SVIQSWLMDVPGFERRWVTRRDAQDSLQVFNVAAYPDYNDHPLMGVDLHWFGARQKLVAVDFQBLVQ- : 60
YHP2_PROMA : -----MNKMLQDLHNNLKRRI-ISHGKPIEVENGMSERFSHKQD- : 40
YHP3_PROMA : -----MIKRDNSLSKIDLRDWIWTFFNDLVDKL-SVFEIEEPVPSHDFLSKESITGSR : 54
YCP3_SYNPY : -----MTNQRFKSTDPVNIEGWSWQPFLEDAIKRL-EGLNVEEPYVPDRFLQREDQTGSK : 54
SLR0116 : -----NAVTDLSLTNSSLMPTLNPMIQQLALATAASW-QSLPLKEYPQLPEDLGYVEGRLEGE : 56
* 20 * 40 * 60 * 80
P 5
HY2 ARATH : -----TELQMLAEKSSKIRLIRSMATHEN-ETMQVFFDFAGEMEPEYDTPLECANFETSTNVN- -HVVLDLNLHQLTDQTDYQDKVYN : 160
YCP2_SYNPY : -----SVIQSWLMDVPGFERRWVTRRDAQDSLQVFNVAAYPDYNDHPLMGVDLHWFGARQKLVAVDFQBLVQ- : 165
YHP2_PROMA : -----TVIKSWLMDVPGFERRWVTRRDAQDSLQVFNVAAYPDYNDHPLMGVDLHWFGARQKLVAVDFQBLVQ- : 115
YHP3_PROMA : -----RNPVHTTLTAAKFEKIKQVRLACIKGCESSVFNLIHPLNDYDLPEFCADFTLPGN- -HMLALDQDQAKL- -DNHTENVMP : 119
YCP3_SYNPY : -----SKSIPVTTATWACKTEKEKQVRLACIKGCESSVFNLIHPLNDYDLPEFCADFTLPGN- -HMLALDQDQAKL- -DNHTENVMP : 137
SLR0116 : -----K- - -LVJENRCYQTPQEPKMHIELAKVCKGFDLHCVMEPEPLYGLPLEGCDIVAGPGG-VSAATADLSEPTQS- - -DRQLPAAAYOK : 135
* 100 * 120 * 140 * 160 *
4 r g 6 p y p g 1
HY2 ARATH : -----SITHKKAETFEWGCKLTGESIKFTSPLVMTTR- - -FSKSEKHKALFSALEYYQALLETIOVRBEMEPESHVRANCEA : 240
YCP2_SYNPY : -----EINQREPDINGEETMRSFDPNQVSSWLLFCR- - -GGAEQADLSIPKAFSALEKAYWDLDHNAKSPSTIPPEEVKNL : 244
YHP2_PROMA : -----DIQ- - -ITKNRRVDNFSQKTNKIYDSNRKFSSEWVLLYN- - -GSFDDQLQCSIAKILDEFTHAHWQVNNNSREYIKIIPSKVQNL : 193
YHP3_PROMA : -----RMI- - -PHDHMQSLLPSSGEIPKEAEPYPSGFLMSRLPLSKESDNIISEIMRPNFEGEXLSLYIELHLIAKPKKKER-ALAKILEG : 197
YCP3_SYNPY : -----RMI- - -PIFERMDQLPYGPGPIPEEAQPFSEGFMTWRLPLGEEGDELIQSIVRPAENDYTDLLLELAASAEPVTDER-SEVTLQG : 219
SLR0116 : -----SLAELGQPEFEQORELPDWC- - -EIESEYCLFIR- - -PSNVTEERFVQVRVVDLQIHCHQSIVAEPISEAQ-TLEHRQG : 208
* 180 * 200 * 220 * 240 * 260
6 FS 6 r 51
HY2 ARATH : -----QHKYLTWRAQKDBGHGELRRLVCEAKAKELRDRDFLNGVDELGKTKTFIDYFPEYQTEDGTVSDKRSIIGKSYETRPWDLTGQFIG : 320
YCP2_SYNPY : -----QDKYDIYSAERDPAHGLFTSHFCKDTSNRRELHEFLFPASSSHK- : 329
YHP2_PROMA : -----HINXDIYSAERDPAHGLFKSYECQTMADQEVREKLEPHSHLTAD- : 236
YHP3_PROMA : -----QKATINRSTKDDPARMLCRFCKEWTEDMHHVLFNI- : 241
YCP3_SYNPY : -----QKRYTDYRAEKDPAHGLTRFHGSEMTTEAMIHTVLFDL- : 257
SLR0116 : -----QIHYCQQQQKNDKTRRVLEKAECEACERMSQVLEDDVIQ- : 257
q Y Dp 6 G W 6 LF
* 280 * 300 * 320 * 340

Fig. 5

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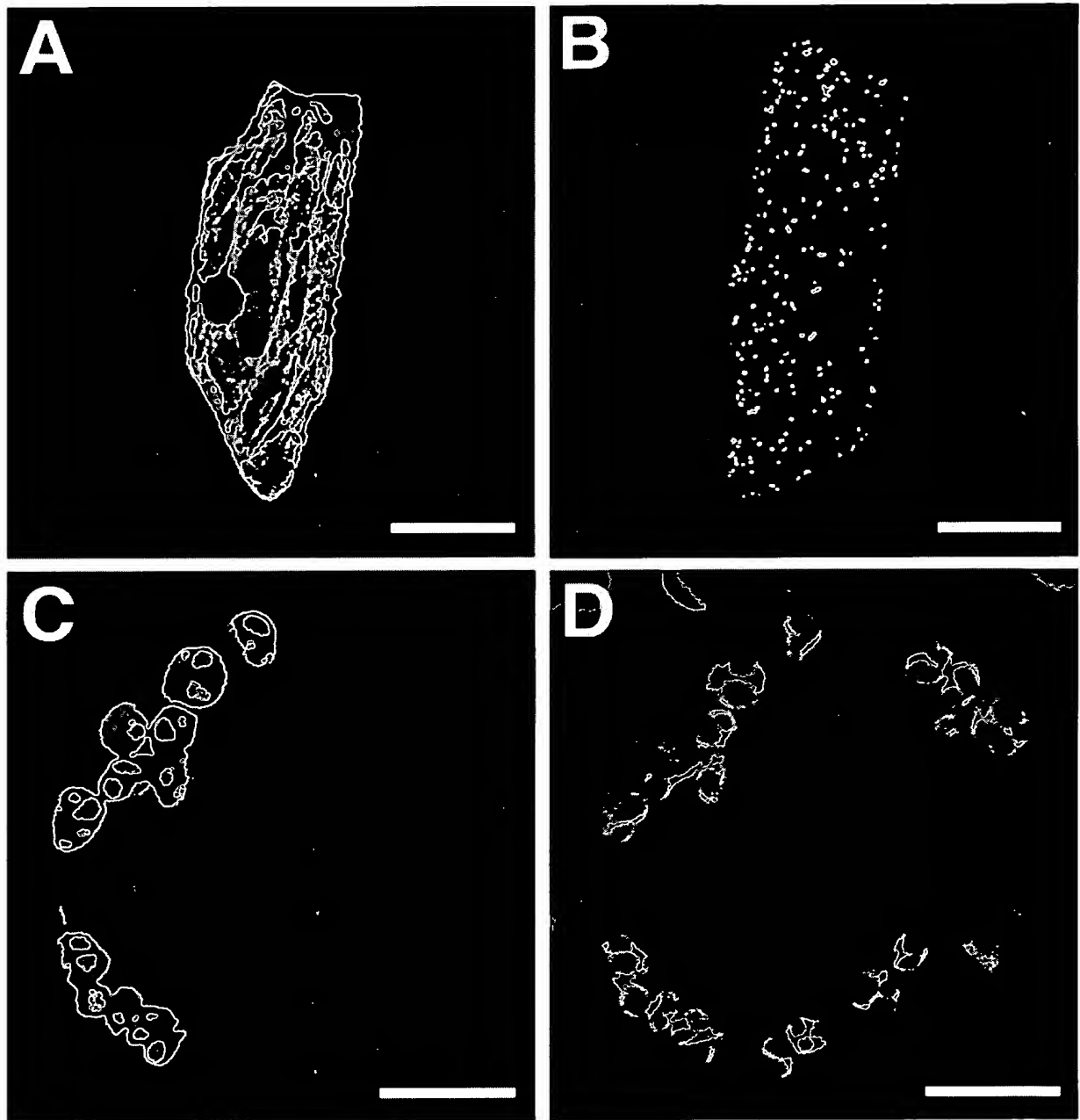


Fig. 6

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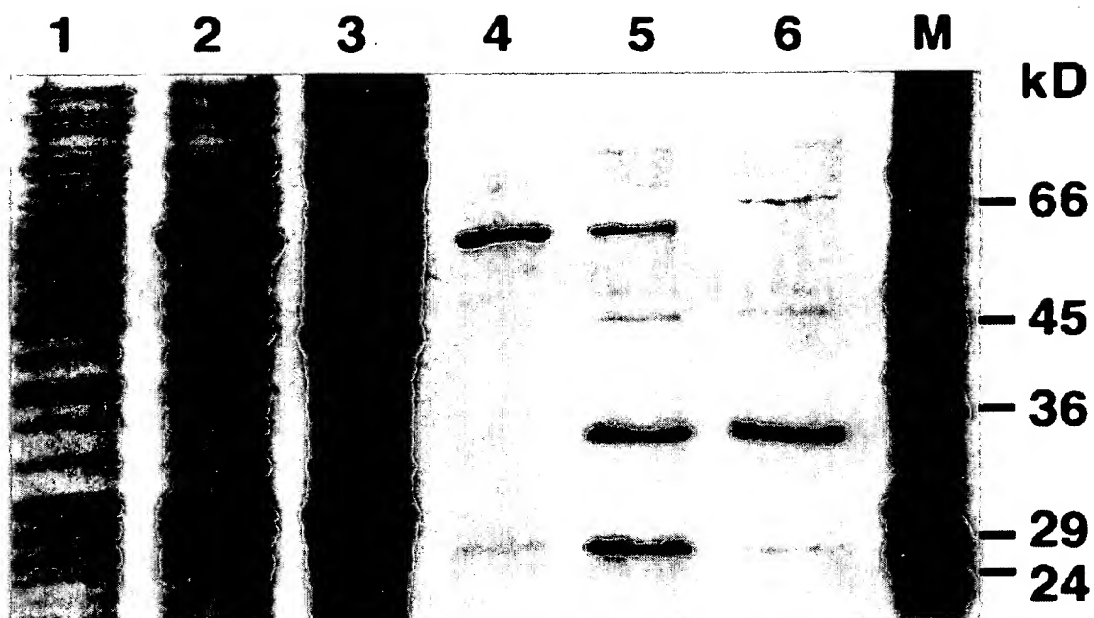


Fig. 7

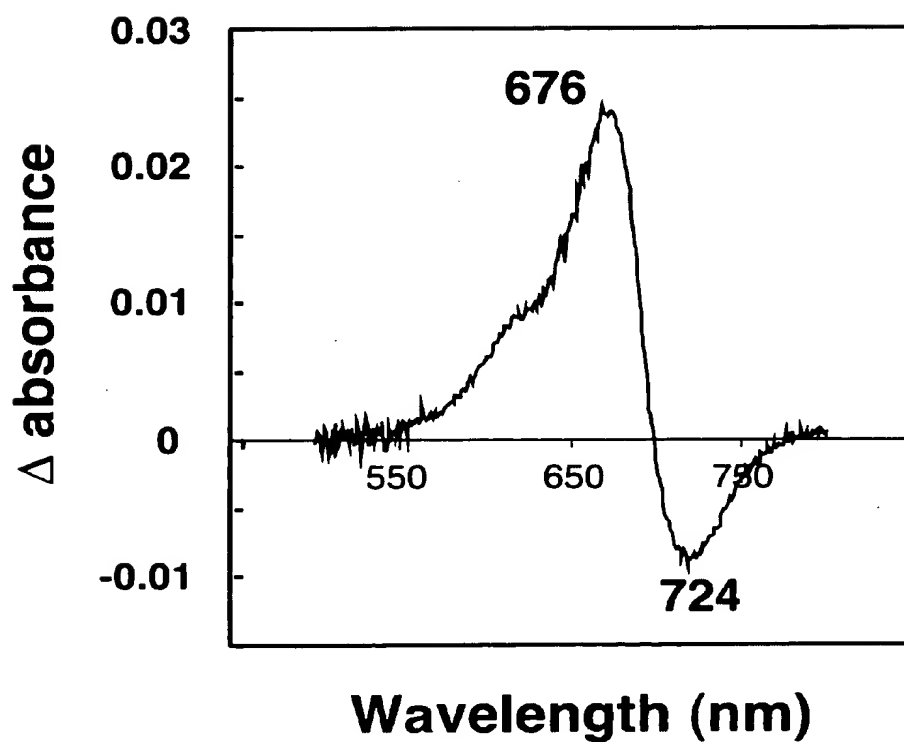


Fig. 8

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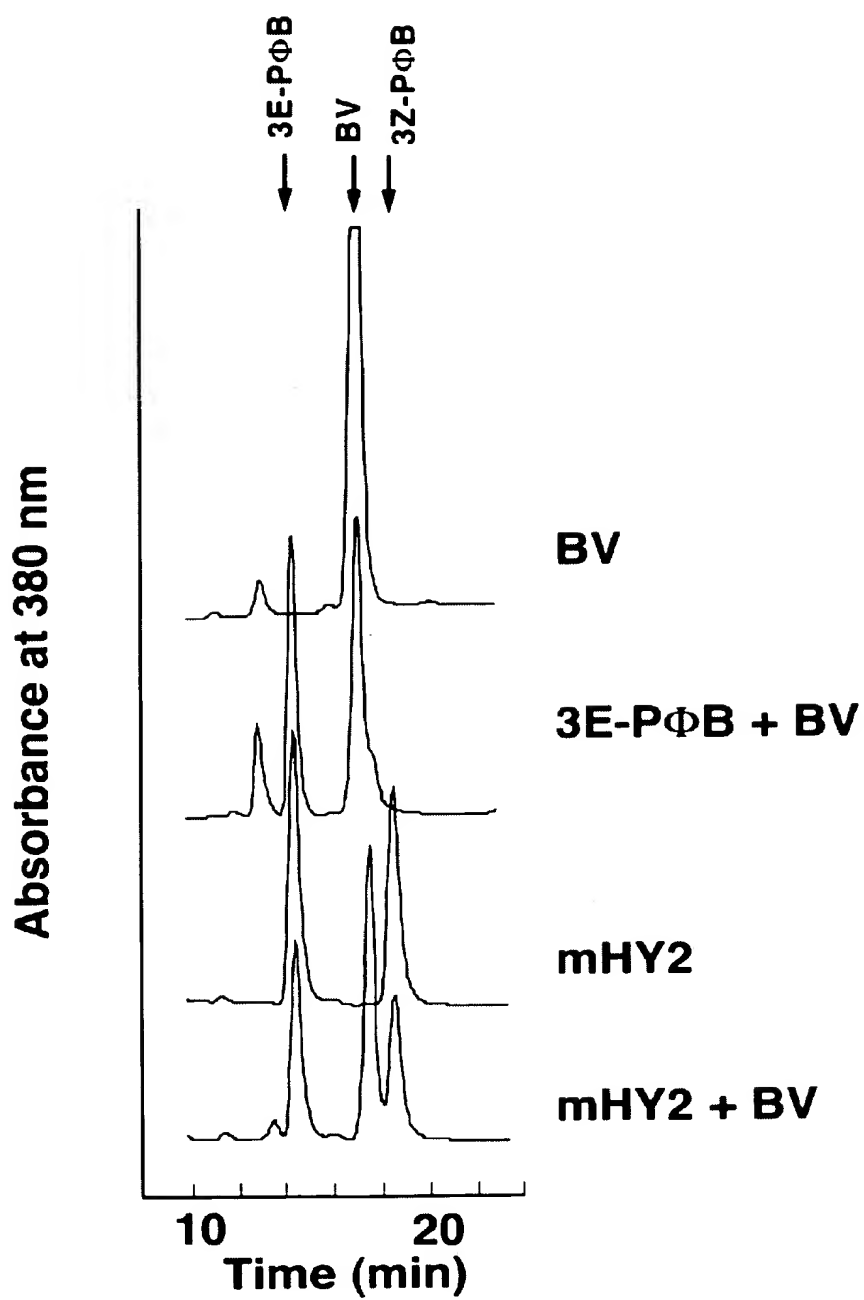


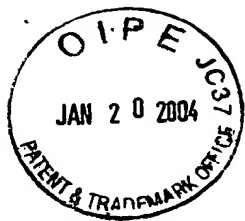
Fig. 9

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[illegible]

Fig. 10A

[illegible]



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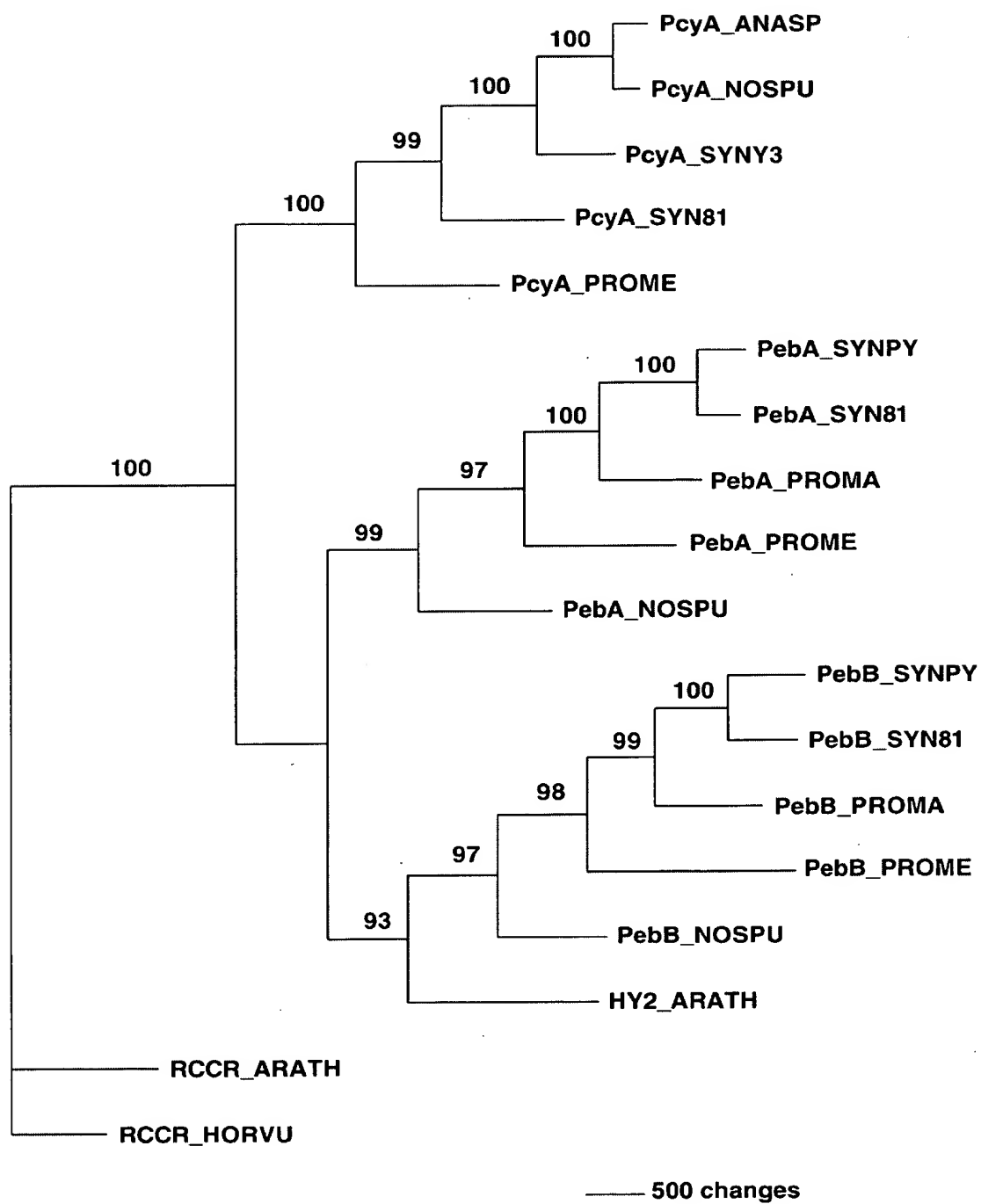


Fig. 11

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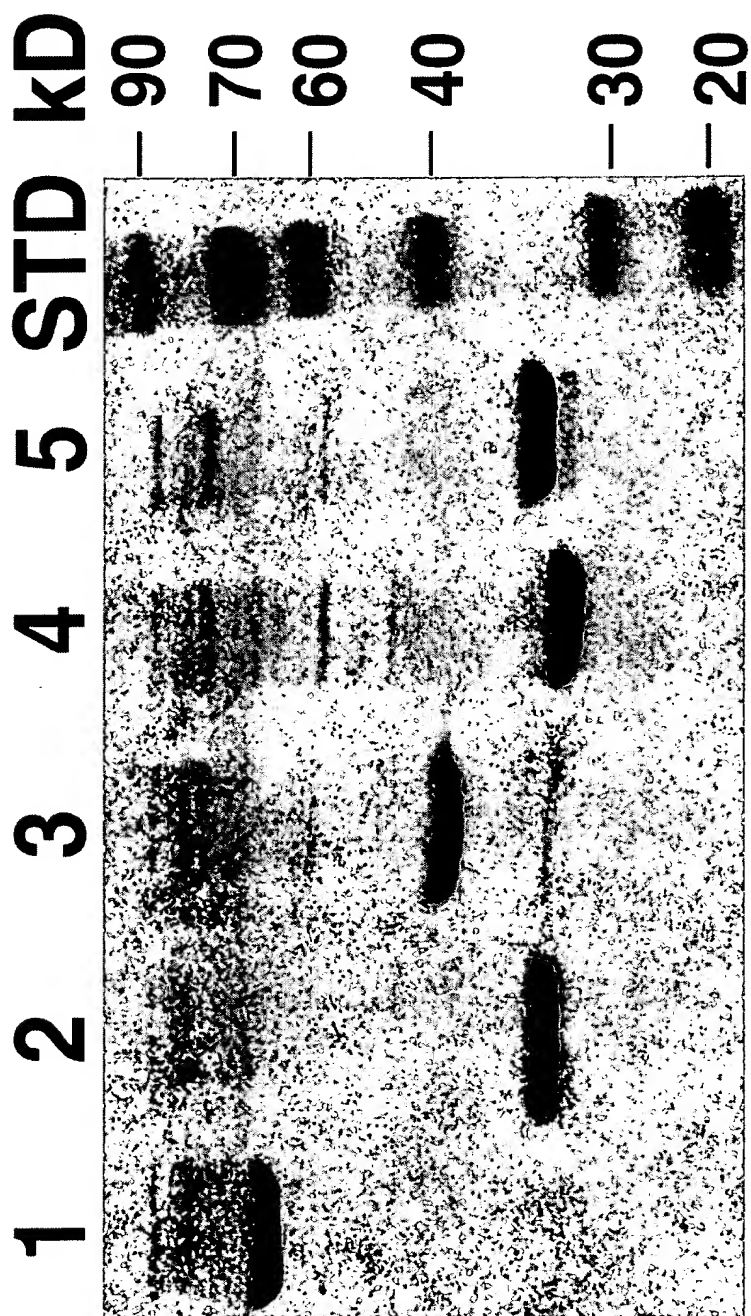


Fig. 12



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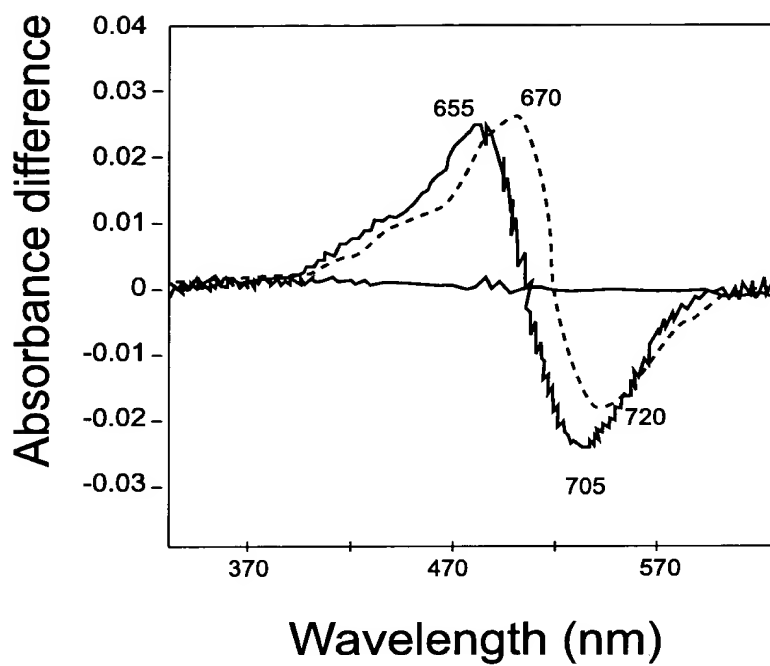


Fig. 13A

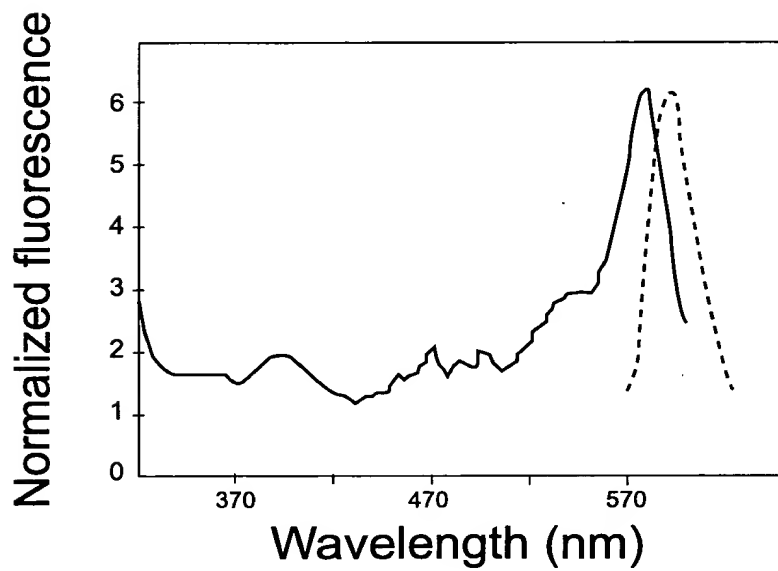


Fig. 13B

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Relative absorbance

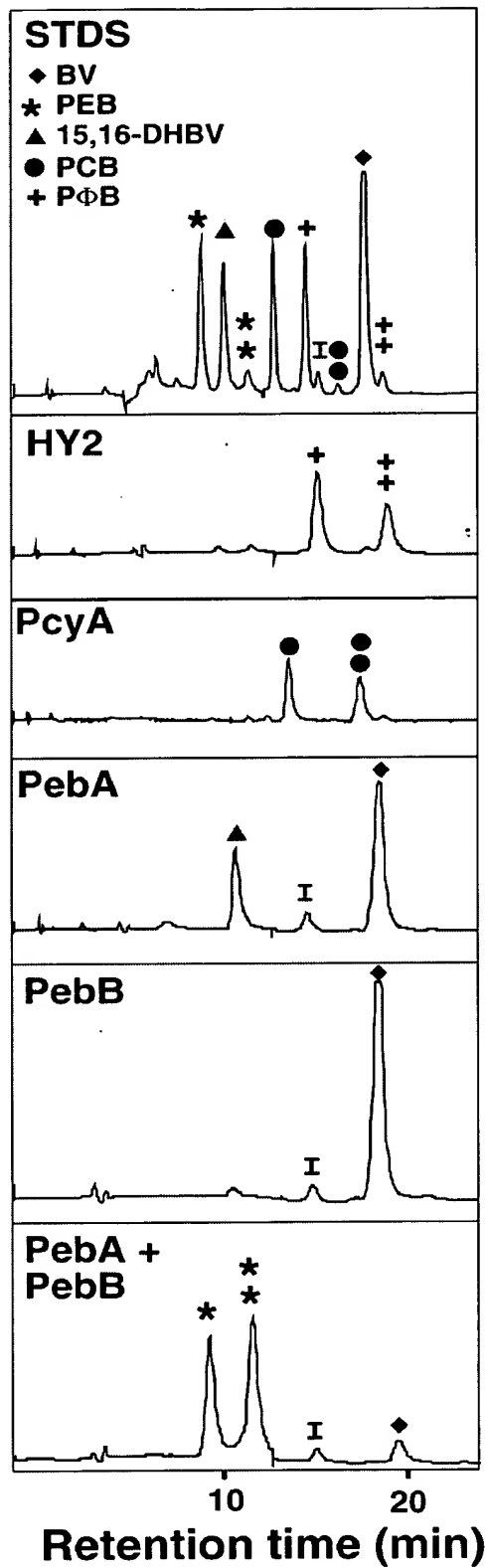


Fig. 14

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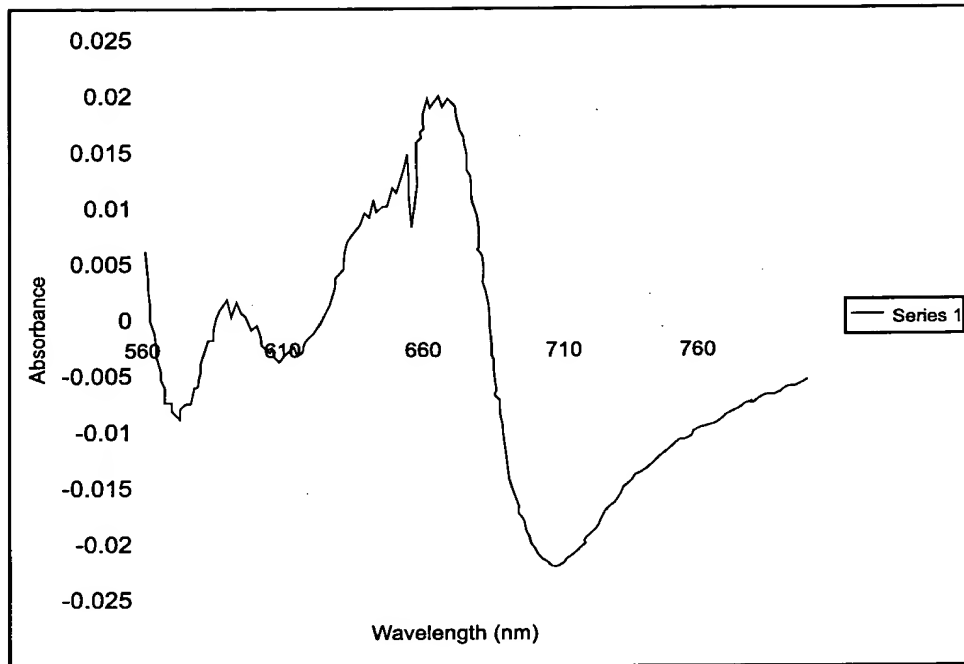


Fig. 15

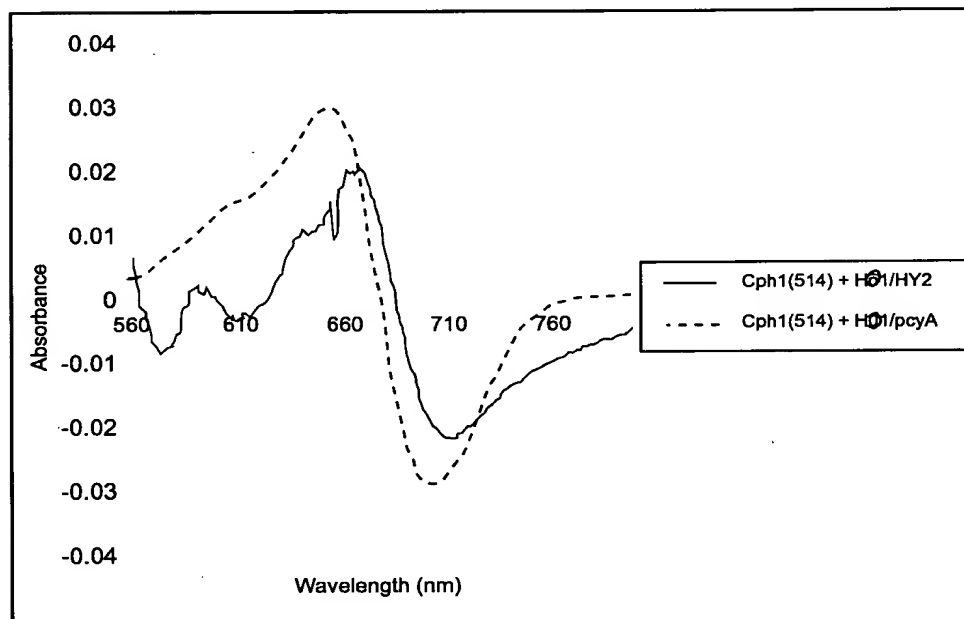


Fig. 16